

SEQ ID NOS. 16-19 to the sequences illustrated in FIG. 2, and submit herewith full sequence listings for the sequences illustrated in FIG. 2, in both paper form and computer readable form. Applicants, through their Attorneys of Record, hereby certify that the paper copy of the sequence listings is a full and accurate representation of the computer readable copies of the sequence listings. Applicants urge that the current response, along with the response mailed on March 25, 2002, are fully responsive to the Office Action mailed on October 4, 2001.

CONCLUSION

It is submitted that claims 7-9, as amended, are in condition for allowance. Early and favorable action by the Examiner is earnestly solicited. In addition, Applicants reserve the right to file a continuing or divisional application to further prosecute claims 17-18, 24, 41, 44, and 58-59, withdrawn from consideration by the Examiner. If the Examiner believes that issues may be resolved by a telephone interview, the Examiner is respectfully urged to telephone the undersigned at (212) 801-2146. The undersigned may also be contacted by e-mail at ecr@gtlaw.com.

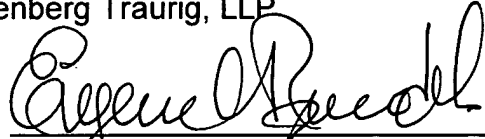
AUTHORIZATION

No fee is believed due for this amendment.

Date: July 24, 2002

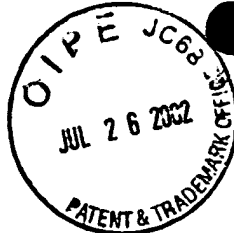
Respectfully submitted,
Greenberg Traurig, LLP

By:



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are indicated in bold. A potential N-glycosylation site is double underlined.

Figure 2: (SEQ ID NOS. 16, 17, 18, and 19) is alignment
5 of the predicted mature protein sequences of human GDNF, NTN,
PSP and EVN. The sequences were aligned using the ClustalW
alignment program. Amino acid residues conserved between all
three proteins are included in the black areas. Residues
conserved between two or three of the sequences are shaded in
10 grey. The 7 conserved cysteine residues characteristic for
members of the TGF- β family are indicated by asterisks above
the sequence. Amino acid residues are numbered to the right.
The dashes indicate gaps introduced into the sequence to
optimize the alignment.

15 Figure 3: (SEQ ID NO. 5) is partial cDNA sequence of
enovin. The consensus sequence was obtained by PCR
amplification (primary PCR with primers PNHsp1 and PNHap1 and
nested PCR with primers PNHsp2 and PNHap2) on different cDNAs
followed by cloning and sequence analysis and comparison of
20 the obtained sequences. The translated one letter code amino
acid sequence of nucleotides 30 to 284 (reading frame A) is
shown above the sequence and numbered to the right (A1 to
A85). This reading frame contains a putative ATG translation
start codon. The translated one letter code amino acid
25 sequence of nucleotides 334 to 810 (reading frame B) is shown
above the sequence and numbered to the right (B1 to B159).
This reading frame contains the region of homology with GDNF,
NTN and PSP. The nucleotide residue number is shown to the
right of the DNA sequence. The putative RXXR cleavage site
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